CLAIMS AMENDMENT

Claims 1-16. (Canceled).

Claim 17. (Previously Presented). A method for detecting a target nucleic acid sequence suspected of having single or large deletions or insertions in a test sample comprising the steps of:

a) contacting the test sample with amplification reagents comprising a polymerase, a primer pair, and a probe to form a reaction mixture;

b) performing the following cycle comprising the steps of:

(i) maintaining the reaction mixture for a time and at temperature above 90°C, sufficient to dissociate double stranded nucleic acid sequences,

(ii) maintaining the reaction mixture for a time and at a temperature from 45°C to 65°C to allow the primers and probe to hybridize to the nucleic acid and thereby form primer hybrids and probe hybrids,

(iii) maintaining the reaction mixture for a time and at a temperature at least 1°C above the temperature in (ii), sufficient to dissociate the probe hybrids, if the probe is not completely complementary to the nucleic acid, and

(iv) raising the temperature of the reaction mixture to a temperature sufficient to activate the polymerase;

c) repeatedly performing the cycle of step b) to form an amplification product; and

d) detecting the amplification product as an indication of the presence of the nucleic acid sequence in the test sample.

Claim 18. (Previously Presented). The method of claim 17 wherein the target nucleic acid sequence is a polymorphic nucleic acid sequence.

Claims 19-37. (Canceled).

Claim 38. (Previously Amended). A method for determining whether a deletion or insertion of at least 50 base pairs is present in DNA in a test sample comprising the steps of:

a) contacting the test sample with amplification reagents to form a reaction mixture, wherein the amplification reagents comprise amplification primers;

b) subjecting the reaction mixture to amplification conditions to form a target nucleic acid sequence amplification product, if the target nucleic acid is present in the test sample, and a standard nucleic acid amplification product;

c) detecting a first signal that is proportional to the amount of the target nucleic acid sequence amplification product;

d) detecting a second signal that is proportional to the amount of the standard nucleic acid amplification product; and

e) comparing the first signal to the second signal to determine whether a deletion or insertion of at least 50 base pairs is present in the DNA in the test sample, wherein the amplification reagents comprise one primer that hybridizes to both the target nucleic acid sequence and the standard nucleic acid sequence.

Claim 39. (Previously Presented). The method of claim 38 wherein the deletion or insertion is of at least 200 base pairs.

Claim 40. (Previously Presented). The method of claim 38 wherein the deletion or insertion is of at least 1000 base pairs.

Claim 41. (Canceled).

Claim 42. (Canceled).

Claim 43. (Previously presented). The method of claim 38 wherein the insertion or deletion is in the CYP2D6 locus.

Claim 44. (Previously Presented). The method of claim 38, wherein the amplification reagents further comprise a polymerase.

Claim 45. (Previously Presented). The method of claim 44, wherein the amplification conditions comprise performing the following cycle comprising the steps of:

(i) maintaining the reaction mixture for a time and at temperature above 90°C, sufficient to dissociate double stranded DNA sequences,

(ii) maintaining the reaction mixture for a time and at a temperature from 45°C to 65°C to allow the amplification primers and probe to hybridize to the DNA and thereby form primer hybrids, and

(iii) raising the temperature of the reaction mixture to a temperature sufficient to activate the polymerase.

Claim 46. (Previously Presented). The method of claim 38, wherein the amplification reagents further comprise a polymerase and a probe.

Claim 47. (Previously Presented). The method of claim 46, wherein the amplification conditions comprise performing the following cycle comprising the steps of:

(i) maintaining the reaction mixture for a time and at temperature above 90°C, sufficient to dissociate double stranded DNA sequences,

(ii) maintaining the reaction mixture for a time and at a temperature from 45°C to 65°C to allow the primers and probe to hybridize to the DNA and thereby form primer hybrids and probe hybrids,

(iii) maintaining the reaction mixture for a time and at a temperature at least 1°C above the temperature in (ii), sufficient to dissociate the probe hybrids, if the probe is not completely complementary to the DNA, and

(iv) raising the temperature of the reaction mixture to a temperature sufficient to activate the polymerase.